



SEQUENCE LISTING

<110> ROJER, EVA

<120> REARRANGED SQUAMOUS CELL CARCINOMA ANTIGEN GENES II

<130> 7274

<140> 10/661,742

<141> 2003-09-12

<150> PCT/SE02/00512

<151> 2002-03-15

<150> SE 0100938

<151> 2001-03-15

<160> 19

<170> PatentIn Ver. 3.3

<210> 1

<211> 390

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic construct

<400> 1

Met Asn Ser Leu Ser Glu Ala Asn Thr Lys Phe Met Phe Asp Leu Phe
1 5 10 15

Gln Gln Phe Arg Lys Ser Lys Glu Asn Asn Ile Phe Tyr Ser Pro Ile
20 25 30

Ser Ile Thr Ser Ala Leu Gly Met Val Leu Leu Gly Ala Lys Asp Asn
35 40 45

Thr Ala Gln Gln Ile Lys Lys Val Leu His Phe Asp Gln Val Thr Glu
50 55 60

Asn Thr Thr Gly Lys Ala Ala Thr Tyr His Val Asp Arg Ser Gly Asn
65 70 75 80

Val His His Gln Phe Gln Lys Leu Leu Thr Glu Phe Asn Lys Ser Thr
85 90 95

Asp Ala Tyr Glu Leu Lys Ile Ala Asn Lys Leu Phe Gly Glu Lys Thr
100 105 110

Tyr Leu Phe Leu Gln Glu Tyr Leu Asp Ala Ile Lys Lys Phe Tyr Gln
115 120 125

Thr Ser Val Glu Ser Val Asp Phe Ala Asn Ala Pro Glu Glu Ser Arg
130 135 140

Lys Lys Ile Asn Ser Trp Val Glu Ser Gln Thr Asn Glu Lys Ile Lys
 145 150 155 160
 Asn Leu Ile Pro Glu Gly Asn Ile Gly Ser Asn Thr Thr Leu Val Leu
 165 170 175
 Val Asn Ala Ile Tyr Phe Lys Gly Gln Trp Glu Lys Lys Phe Asn Lys
 180 185 190
 Glu Asp Thr Lys Glu Glu Lys Phe Trp Pro Asn Lys Asn Thr Tyr Lys
 195 200 205
 Ser Ile Gln Met Met Arg Gln Tyr Thr Ser Phe His Phe Ala Ser Leu
 210 215 220
 Glu Asp Val Gln Ala Lys Val Leu Glu Ile Pro Tyr Lys Gly Lys Asp
 225 230 235 240
 Leu Ser Met Ile Val Leu Leu Pro Asn Glu Ile Asp Gly Leu Gln Lys
 245 250 255
 Leu Glu Glu Lys Leu Thr Ala Glu Lys Leu Met Glu Trp Thr Ser Leu
 260 265 270
 Gln Asn Met Arg Glu Thr Cys Val Asp Leu His Leu Pro Arg Phe Lys
 275 280 285
 Met Glu Glu Ser Tyr Asp Leu Lys Asp Thr Leu Arg Thr Met Gly Met
 290 295 300
 Val Asn Ile Phe Asn Gly Asp Ala Asp Leu Ser Gly Met Thr Trp Ser
 305 310 315 320
 His Gly Leu Ser Val Ser Lys Val Leu His Lys Ala Phe Val Glu Val
 325 330 335
 Thr Glu Glu Gly Val Glu Ala Ala Ala Thr Ala Val Val Val Val
 340 345 350
 Glu Leu Ser Ser Pro Ser Thr Asn Glu Glu Phe Cys Cys Asn His Pro
 355 360 365
 Phe Leu Phe Phe Ile Arg Gln Asn Lys Thr Asn Ser Ile Leu Phe Tyr
 370 375 380
 Gly Arg Phe Ser Ser Pro
 385 390

<210> 2

<211> 1193

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic construct

```

<400> 2
atgaattcac tcagtgaagc caacaccaag ttcatgttcg acctgttcca acagttcaga 60
aaatcaaaaag agaacaacat cttctattcc cctatcagca tcacatcagc attagggatg 120
gtcctcttag gagccaaaaga caacactgca caacagatta agaaggttct tcactttgat 180
caagtcacag agaaccaccac aggaaaagct gcaacatatc atgttgatag gtcaggaaat 240
gttcatcacc agtttcaaaa gcttctgact gaattcaaca aattccactg atgcatatga 300
gctgaagatc gccacaagc tcttcggaga aaaaacgtat ctatttttac aggaatatatt 360
agatgccatc aagaaatttt accagaccag tgtggaatct gttgattttg caaatgctcc 420
agaagaaagt cgaaagaaga ttaactcctg ggtggaaagt caaacgaatg aaaaaattaa 480
aaacctaatt cctgaaggta atattggcag caataccaca ttggttcttg tgaacgcaat 540
ctatttcaaa gggcagtggg agaagaaatt taataaagaa gatactaaag aggaaaaatt 600
ttggccaaac aagaatacat acaagtccat acagatgatg aggcaatata catcttttca 660
ttttgcctcg ctggaggatg tacaggccaa ggtcctggaa ataccataca aaggcaaaga 720
tctaagcatg attgtgttgc tgccaaatga aatcgatggt ctccagaagc ttgaagagaa 780
actcactgct gagaaattga tggaatggac aagtttgcag aatatgagag agacatgtgt 840
cgatttacac ttacctcgtt tcaaaatgga agagagctat gacctcaagg acacgttgag 900
aaccatggga atggtgaata tcttcaatgg ggatgcagac ctctcaggca tgacctggag 960
ccacggtctc tcagtatcta aagtcctaca caaggccttt gtggagggtca ctgaggaggg 1020
agtgaagct gcagctgcca ccgctgtagt agtagtcgaa ttatcatctc cttcaactaa 1080
tgaagagttc tgttgtaatc accctttcct attcttcata aggcaaaata agaccaacag 1140
catcctcttc tatggcagat tctcatcccc atagatgcaa ttagtgtgtc act 1193

```

```

<210> 3
<211> 29
<212> DNA
<213> Artificial Sequence

```

```

<220>
<223> Description of Artificial Sequence: Synthetic
      primer

```

```

<400> 3
cgggatccat gaattcactc agtgaagcc 29

```

```

<210> 4
<211> 38
<212> DNA
<213> Artificial Sequence

```

```

<220>
<223> Description of Artificial Sequence: Synthetic
      primer

```

```

<400> 4
gagctcgagt ctcacagtg acagactaat tgcattca 38

```

```

<210> 5
<211> 20
<212> DNA
<213> Artificial Sequence

```

```

<220>
<223> Description of Artificial Sequence: Synthetic
      primer

```

<400> 5
tggaatggac aagtttgcag 20

<210> 6
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
primer

<400> 6
gtaggactcc agatagcac 19

<210> 7
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
primer

<400> 7
tggagccacg gtctctcag 19

<210> 8
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
primer

<400> 8
attagttgaa ggagatgata attc 24

<210> 9
<211> 16
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
primer

<400> 9
aatacataca agtcca 16

<210> 10
 <211> 16
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic primer

<400> 10
 ggacttttaga tactga

16

<210> 11
 <211> 1170
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic construct

<400> 11
 atgaattcac tcagtgaagc caacaccaag ttcattgttcg acctgttcca acagttcaga 60
 aaatcaaaaag agaacaacat cttctattcc cctatcagca tcacatcagc attaggggatg 120
 gtcctcttag gagccaaaga caacactgca caacagatta agaagggttct tcactttgat 180
 caagtccacag agaaccaccac aggaaaagct gcaacatatac atgttgatag gtcaggaaaat 240
 gttcatcacc agtttcaaaa gcttctgact gaattcaaca aatccactga tgcataatgag 300
 ctgaagatcg ccaacaagct cttcggagaa aaaacgtatc tatttttaca ggaatattta 360
 gatgccatca agaaatttta ccagaccagt gtggaatctg ttgattttgc aaatgctcca 420
 gaagaaagtc gaaagaagat taactcctgg gtggaaagtc aaacgaatga aaaaattaaa 480
 aacctaattc ctgaaggtaa tattggcagc aataccacat tgggtcttgt gaacgcaatc 540
 tatttcaaag ggcaagtggga gaagaaattt aataaagaag atactaaaga ggaaaaattt 600
 tggccaaaca agaatacata caagtccata cagatgatga ggcaatacac atcttttcat 660
 tttgcctcgc tggaggatgt acaggccaag gtccctggaaa taccatacaa aggcaaagat 720
 ctaagcatga ttgtgttgct gccaaatgaa atcgatggtc tccagaagct tgaagagaaa 780
 ctactgctg agaaattgat ggaatggaca agtttgcaga atatgagaga gacatgtgtc 840
 gatttacact tacctcggtt caaaatggaa gagagctatg acctcaagga cacgttgaga 900
 accatgggaa tggatgaatat cttcaatggg gatgcagacc tctcaggcat gacctggagc 960
 cacggtctct cagtatctaa agtcctacac aaggcctttg tggaggtcac tgaggaggga 1020
 gtggaagctg cagctgccac cgctgtagta gtatgcgaat tatcatctcc ttcaactaat 1080
 gaagagttct gttgtaatac ccctttccta ttcttcataa ggcaaaaataa gaccaacagc 1140
 atcctcttct atggcagatt ctcattcccca 1170

<210> 12
 <211> 1173
 <212> DNA
 <213> Homo sapiens

<400> 12
 atgaattcac tcagtgaagc caacaccaag ttcattgttcg acctgttcca acagttcaga 60
 aaatcaaaaag agaacaacat cttctattcc cctatcagca tcacatcagc attaggggatg 120
 gtcctcttag gagccaaaga caacactgca caacagatta agaagggttct tcactttgat 180
 caagtccacag agaaccaccac aggaaaagct gcaacatatac atgttgatag gtcaggaaaat 240
 gttcatcacc agtttcaaaa gcttctgact gaattcaaca aatccactga tgcataatgag 300
 ctgaagatcg ccaacaagct cttcggagaa aaaacgtatc tatttttaca ggaatattta 360
 gatgccatca agaaatttta ccagaccagt gtggaatctg ttgattttgc aaatgctcca 420

```

gaagaaagtc gaaagaagat taactcctgg gtggaaagtc aaacgaatga aaaaattaaa 480
aacctaattc ctgaaggtaa tattggcagc aataccacat tggttcttgt gaacgcaatc 540
tatttcaaag ggcagtggga gaagaaattt aataaagaag atactaaaga ggaaaaattt 600
tggccaaaca agaatacata caagtccata cagatgatga ggcaatacac atcttttcat 660
tttgccctgc tggaggatgt acaggccaag gtccctggaaa taccatacaa aggcaaagat 720
ctaagcatga ttgtgttgct gccaaatgaa atcgatggtc tccagaagct tgaagagaaa 780
ctcactgctg agaaattgat ggaatggaca agtttgcaga atatgagaga gacacgtgtc 840
gatttacact tacctcgggt caaagtggaa gagagctatg acctcaagga cacgttgaga 900
accatgggaa tgggtggatat cttcaatggg gatgcagacc tctcaggcat gaccgggagc 960
cgcggtctcg tgctatctgg agtcctacac aaggcctttg tggagggttac agaggaggga 1020
gcagaagctg cagctgccac cgctgtagta ggattcggat catcacctac ttcaactaat 1080
gaagagttcc attgtaatca ccctttccta ttcttcataa ggcaaaaataa gaccaacagc 1140
atcctcttct atggcagatt ctcatccccg tag 1173

```

```

<210> 13
<211> 1173
<212> DNA
<213> Homo sapiens

```

```

<400> 13
atgaattcac tcagtgaagc caacaccaag ttcatgttcg atctgttcca acagttcaga 60
aaatcaaaag agaacaacat cttctattcc cctatcagca tcacatcagc attagggatg 120
gtcctcttag gagccaaaga caacactgca caacaaatta gcaaggttct tcactttgat 180
caagtcacag agaacaccac agaaaaagct gcaacatata atgttgatag gtcagggaat 240
gttcatcacc agtttcaaaa gcttctgact gaattcaaca aatccactga tgcatatgag 300
ctgaagatcg ccaacaagct cttcggagaa aagacgtatc aattttttaca ggaatattta 360
gatgccatca agaaatttta ccagaccagt gtggaatcta ctgattttgc aaatgctcca 420
gaagaaagtc gaaagaagat taactcctgg gtggaaagtc aaacgaatga aaaaattaaa 480
aacctatttc ctgatgggac tattggcaat gatacgacac tggttcttgt gaacgcaatc 540
tatttcaaag ggcagtggga gaataaattt aaaaaagaaa aactaaaga ggaaaaattt 600
tggccaaaca agaatacata caaatctgta cagatgatga ggcaatacaa ttcctttaat 660
tttgccctgc tggaggatgt acaggccaag gtccctggaaa taccatacaa aggcaaagat 720
ctaagcatga ttgtgctgct gccaaatgaa atcgatggtc tgcagaagct tgaagagaaa 780
ctcactgctg agaaattgat ggaatggaca agtttgcaga atatgagaga gacatgtgtc 840
gatttacact tacctcgggt caaaatggaa gagagctatg acctcaagga cacgttgaga 900
accatgggaa tgggtgaatat cttcaatggg gatgcagacc tctcaggcat gaccgggagc 960
cacggtctct cagtatctaa agtcctacac aaggcctttg tggagggtcac tgaggaggga 1020
gtggaagctg cagctgccac cgctgtagta gtagtcgaat tatcatctcc ttcaactaat 1080
gaagagttct gttgtaatca ccctttccta ttcttcataa ggcaaaaataa gaccaacagc 1140
atcctcttct atggcagatt ctcatcccca tag 1173

```

```

<210> 14
<211> 390
<212> PRT
<213> Homo sapiens

```

```

<400> 14
Met Asn Ser Leu Ser Glu Ala Asn Thr Lys Phe Met Phe Asp Leu Phe
  1                      5                      10                      15

Gln Gln Phe Arg Lys Ser Lys Glu Asn Asn Ile Phe Tyr Ser Pro Ile
          20                      25                      30

Ser Ile Thr Ser Ala Leu Gly Met Val Leu Leu Gly Ala Lys Asp Asn
    35                      40                      45

```

Thr	Ala	Gln	Gln	Ile	Lys	Lys	Val	Leu	His	Phe	Asp	Gln	Val	Thr	Glu	50	55	60
Asn	Thr	Thr	Gly	Lys	Ala	Ala	Thr	Tyr	His	Val	Asp	Arg	Ser	Gly	Asn	65	70	75
Val	His	His	Gln	Phe	Gln	Lys	Leu	Leu	Thr	Glu	Phe	Asn	Lys	Ser	Thr	85	90	95
Asp	Ala	Tyr	Glu	Leu	Lys	Ile	Ala	Asn	Lys	Leu	Phe	Gly	Glu	Lys	Thr	100	105	110
Tyr	Leu	Phe	Leu	Gln	Glu	Tyr	Leu	Asp	Ala	Ile	Lys	Lys	Phe	Tyr	Gln	115	120	125
Thr	Ser	Val	Glu	Ser	Val	Asp	Phe	Ala	Asn	Ala	Pro	Glu	Glu	Ser	Arg	130	135	140
Lys	Lys	Ile	Asn	Ser	Trp	Val	Glu	Ser	Gln	Thr	Asn	Glu	Lys	Ile	Lys	145	150	155
Asn	Leu	Ile	Pro	Glu	Gly	Asn	Ile	Gly	Ser	Asn	Thr	Thr	Leu	Val	Leu	165	170	175
Val	Asn	Ala	Ile	Tyr	Phe	Lys	Gly	Gln	Trp	Glu	Lys	Lys	Phe	Asn	Lys	180	185	190
Glu	Asp	Thr	Lys	Glu	Glu	Lys	Phe	Trp	Pro	Asn	Lys	Asn	Thr	Tyr	Lys	195	200	205
Ser	Ile	Gln	Met	Met	Arg	Gln	Tyr	Thr	Ser	Phe	His	Phe	Ala	Ser	Leu	210	215	220
Glu	Asp	Val	Gln	Ala	Lys	Val	Leu	Glu	Ile	Pro	Tyr	Lys	Gly	Lys	Asp	225	230	235
Leu	Ser	Met	Ile	Val	Leu	Leu	Pro	Asn	Glu	Ile	Asp	Gly	Leu	Gln	Lys	245	250	255
Leu	Glu	Glu	Lys	Leu	Thr	Ala	Glu	Lys	Leu	Met	Glu	Trp	Thr	Ser	Leu	260	265	270
Gln	Asn	Met	Arg	Glu	Thr	Arg	Val	Asp	Leu	His	Leu	Pro	Arg	Phe	Lys	275	280	285
Val	Glu	Glu	Ser	Tyr	Asp	Leu	Lys	Asp	Thr	Leu	Arg	Thr	Met	Gly	Met	290	295	300
Val	Asp	Ile	Phe	Asn	Gly	Asp	Ala	Asp	Leu	Ser	Gly	Met	Thr	Gly	Ser	305	310	315
Arg	Gly	Leu	Val	Leu	Ser	Gly	Val	Leu	His	Lys	Ala	Phe	Val	Glu	Val	325	330	335
Thr	Glu	Glu	Gly	Ala	Glu	Ala	Ala	Ala	Ala	Thr	Ala	Val	Val	Gly	Phe	340	345	350

Gly Ser Ser Pro Ala Ser Thr Asn Glu Glu Phe His Cys Asn His Pro
 355 360 365

Phe Leu Phe Phe Ile Arg Gln Asn Lys Thr Asn Ser Ile Leu Phe Tyr
 370 375 380

Gly Arg Phe Ser Ser Pro
 385 390

<210> 15

<211> 390

<212> PRT

<213> Homo sapiens

<400> 15

Met Asn Ser Leu Ser Glu Ala Asn Thr Lys Phe Met Phe Asp Leu Phe
 1 5 10 15

Gln Gln Phe Arg Lys Ser Lys Glu Asn Asn Ile Phe Tyr Ser Pro Ile
 20 25 30

Ser Ile Thr Ser Ala Leu Gly Met Val Leu Leu Gly Ala Lys Asp Asn
 35 40 45

Thr Ala Gln Gln Ile Ser Lys Val Leu His Phe Asp Gln Val Thr Glu
 50 55 60

Asn Thr Thr Glu Lys Ala Ala Thr Tyr His Val Asp Arg Ser Gly Asn
 65 70 75 80

Val His His Gln Phe Gln Lys Leu Leu Thr Glu Phe Asn Lys Ser Thr
 85 90 95

Asp Ala Tyr Glu Leu Lys Ile Ala Asn Lys Leu Phe Gly Glu Lys Thr
 100 105 110

Tyr Gln Phe Leu Gln Glu Tyr Leu Asp Ala Ile Lys Lys Phe Tyr Gln
 115 120 125

Thr Ser Val Glu Ser Thr Asp Phe Ala Asn Ala Pro Glu Glu Ser Arg
 130 135 140

Lys Lys Ile Asn Ser Trp Val Glu Ser Gln Thr Asn Glu Lys Ile Lys
 145 150 155 160

Asn Leu Phe Pro Asp Gly Thr Ile Gly Asn Asp Thr Thr Leu Val Leu
 165 170 175

Val Asn Ala Ile Tyr Phe Lys Gly Gln Trp Glu Asn Lys Phe Lys Lys
 180 185 190

Glu Asn Thr Lys Glu Glu Lys Phe Trp Pro Asn Lys Asn Thr Tyr Lys
 195 200 205

Ser Val Gln Met Met Arg Gln Tyr Asn Ser Phe Asn Phe Ala Leu Leu
 210 215 220

Glu Asp Val Gln Ala Lys Val Leu Glu Ile Pro Tyr Lys Gly Lys Asp
 225 230 235 240
 Leu Ser Met Ile Val Leu Leu Pro Asn Glu Ile Asp Gly Leu Gln Lys
 245 250 255
 Leu Glu Glu Lys Leu Thr Ala Glu Lys Leu Met Glu Trp Thr Ser Leu
 260 265 270
 Gln Asn Met Arg Glu Thr Cys Val Asp Leu His Leu Pro Arg Phe Lys
 275 280 285
 Met Glu Glu Ser Tyr Asp Leu Lys Asp Thr Leu Arg Thr Met Gly Met
 290 295 300
 Val Asn Ile Phe Asn Gly Asp Ala Asp Leu Ser Gly Met Thr Trp Ser
 305 310 315 320
 His Gly Leu Ser Val Ser Lys Val Leu His Lys Ala Phe Val Glu Val
 325 330 335
 Thr Glu Glu Gly Val Glu Ala Ala Ala Thr Ala Val Val Val Val
 340 345 350
 Glu Leu Ser Ser Pro Ser Thr Asn Glu Glu Phe Cys Cys Asn His Pro
 355 360 365
 Phe Leu Phe Phe Ile Arg Gln Asn Lys Thr Asn Ser Ile Leu Phe Tyr
 370 375 380
 Gly Arg Phe Ser Ser Pro
 385 390

<210> 16

<211> 1173

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic construct

<400> 16

atgaattcac tcagtgaagc caacaccaag ttcattgttcg acctgttcca acagttcaga 60
 aaatcaaaaag agaacaacat cttctattcc cctatcagca tcacatcagc attagggatg 120
 gtcctcttag gagccaaaga caacactgca caacagatta agaaggttct tcactttgat 180
 caagtcacag agaaccaccac aggaaaagct gcaacatata atgttgatag gtcaggaaat 240
 gttcatcacc agtttcaaaa gcttctgact gaattcaaca aatccactga tgcataatgag 300
 ctgaagatcg ccaacaagct cttcggagaa aaaacgtatc tattttttaca ggaatattta 360
 gatgccatca agaaatttta ccagaccagt gtggaaatctg ttgattttgc aaatgctcca 420
 gaagaaagtc gaaagaagat taactcctgg gtggaaagtc aaacgaatga aaaaattaaa 480
 aacctaattc ctgaaggtaa tattggcagc aataccacat tgggtcctgt gaacgcaatc 540
 tatttcaaag ggcagtggga gaagaaattt aataaagaag atactaaaga ggaaaaattt 600
 tggccaaaca agaatacata caartcyrt cagatgatga ggcaatacam wtcytttmat 660
 tttgcttygc tggaggatgt acaggccaag gtcctggaaa taccatacaa aggcaaagat 720
 ctaagcatga ttgtgytgct gccaaatgaa atcgatggtc tscagaagct tgaagagaaa 780
 ctcaactgctg agaaattgat ggaatggaca agtttgcaga atatgagaga gacaygtgtc 840

```

gatttacact tacctcggtt caaartggaa gagagctatg acctcaagga cacgttgaga 900
accatgggaa tggatgratat cttcaatggg gatgcagacc tctcaggcat gacckggagc 960
crcggtctck yrstatctrr agtcctacac aaggcctttg tggaggtyac wgaggaggga 1020
gyrgaagctg cagctgccac cgctgtagta gtagtcgaat tatcatctcc ttcaactaat 1080
gaagagttct gttgtaatca ccctttccta ttcttcataa ggcaaaaataa gaccaacagc 1140
atcctcttct atggcagatt ctcaccccca tag 1173

```

<210> 17

<211> 390

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic construct

<220>

<221> MOD_RES

<222> (210)

<223> Ile or Val

<220>

<221> MOD_RES

<222> (217)

<223> Thr or Asn

<220>

<221> MOD_RES

<222> (220)

<223> His or Asn

<220>

<221> MOD_RES

<222> (223)

<223> Ser or Leu

<220>

<221> MOD_RES

<222> (279)

<223> Arg or Cys

<220>

<221> MOD_RES

<222> (289)

<223> Val or Met

<220>

<221> MOD_RES

<222> (306)

<223> Asp or Asn

<220>

<221> MOD_RES

<222> (319)

<223> Gly or Trp

<220>
 <221> MOD_RES
 <222> (321)
 <223> Arg or His

<220>
 <221> MOD_RES
 <222> (324)
 <223> Val or Ser

<220>
 <221> MOD_RES
 <222> (325)
 <223> Leu or Val

<220>
 <221> MOD_RES
 <222> (327)
 <223> Gly or Lys

<220>
 <221> MOD_RES
 <222> (341)
 <223> Ala or Val

<400> 17

Met	Asn	Ser	Leu	Ser	Glu	Ala	Asn	Thr	Lys	Phe	Met	Phe	Asp	Leu	Phe	1	5	10	15
Gln	Gln	Phe	Arg	Lys	Ser	Lys	Glu	Asn	Asn	Ile	Phe	Tyr	Ser	Pro	Ile	20	25	30	
Ser	Ile	Thr	Ser	Ala	Leu	Gly	Met	Val	Leu	Leu	Gly	Ala	Lys	Asp	Asn	35	40	45	
Thr	Ala	Gln	Gln	Ile	Lys	Lys	Val	Leu	His	Phe	Asp	Gln	Val	Thr	Glu	50	55	60	
Asn	Thr	Thr	Gly	Lys	Ala	Ala	Thr	Tyr	His	Val	Asp	Arg	Ser	Gly	Asn	65	70	75	80
Val	His	His	Gln	Phe	Gln	Lys	Leu	Leu	Thr	Glu	Phe	Asn	Lys	Ser	Thr	85	90	95	
Asp	Ala	Tyr	Glu	Leu	Lys	Ile	Ala	Asn	Lys	Leu	Phe	Gly	Glu	Lys	Thr	100	105	110	
Tyr	Leu	Phe	Leu	Gln	Glu	Tyr	Leu	Asp	Ala	Ile	Lys	Lys	Phe	Tyr	Gln	115	120	125	
Thr	Ser	Val	Glu	Ser	Val	Asp	Phe	Ala	Asn	Ala	Pro	Glu	Glu	Ser	Arg	130	135	140	
Lys	Lys	Ile	Asn	Ser	Trp	Val	Glu	Ser	Gln	Thr	Asn	Glu	Lys	Ile	Lys	145	150	155	160
Asn	Leu	Ile	Pro	Glu	Gly	Asn	Ile	Gly	Ser	Asn	Thr	Thr	Leu	Val	Leu	165	170	175	

Val Asn Ala Ile Tyr Phe Lys Gly Gln Trp Glu Lys Lys Phe Asn Lys
 180 185 190
 Glu Asp Thr Lys Glu Glu Lys Phe Trp Pro Asn Lys Asn Thr Tyr Lys
 195 200 205
 Ser Xaa Gln Met Met Arg Gln Tyr Xaa Ser Phe Xaa Phe Ala Xaa Leu
 210 215 220
 Glu Asp Val Gln Ala Lys Val Leu Glu Ile Pro Tyr Lys Gly Lys Asp
 225 230 235 240
 Leu Ser Met Ile Val Leu Leu Pro Asn Glu Ile Asp Gly Leu Gln Lys
 245 250 255
 Leu Glu Glu Lys Leu Thr Ala Glu Lys Leu Met Glu Trp Thr Ser Leu
 260 265 270
 Gln Asn Met Arg Glu Thr Xaa Val Asp Leu His Leu Pro Arg Phe Lys
 275 280 285
 Xaa Glu Glu Ser Tyr Asp Leu Lys Asp Thr Leu Arg Thr Met Gly Met
 290 295 300
 Val Xaa Ile Phe Asn Gly Asp Ala Asp Leu Ser Gly Met Thr Xaa Ser
 305 310 315 320
 Xaa Gly Leu Xaa Xaa Ser Xaa Val Leu His Lys Ala Phe Val Glu Val
 325 330 335
 Thr Glu Glu Gly Xaa Glu Ala Ala Ala Thr Ala Val Val Val Val
 340 345 350
 Glu Leu Ser Ser Pro Ser Thr Asn Glu Glu Phe Cys Cys Asn His Pro
 355 360 365
 Phe Leu Phe Phe Ile Arg Gln Asn Lys Thr Asn Ser Ile Leu Phe Tyr
 370 375 380
 Gly Arg Phe Ser Ser Pro
 385 390

<210> 18

<211> 1173

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic construct

<400> 18

atgaattcac tcagtgaagc caacaccaag ttcattgttcg atctgttcca acagttcaga 60
 aaatcaaaag agaacaacat cttctattcc cctatcagca tcacatcagc attagggatg 120
 gtcctcttag gagccaaaga caacactgca caacaaatta gcaaggttct tcactttgat 180
 caagtcacag agaacaccac agaaaaagct gcaacatatc atgttgatag gtcaggaaat 240

```

gttcatcacc agtttcaaaa gcttctgact gaattcaaca aatccactga tgcatatgag 300
ctgaagatcg ccaacaagct cttcggagaa aagacgtatc aattttttaca ggaatattta 360
gatgccatca agaaatttta ccagaccagt gtggaatcta ctgattttgc aaatgctcca 420
gaagaaagtc gaaagaagat taactcctgg gtggaaagtc aaacgaatga aaaaattaaa 480
aacctatttc ctgatgggac tattggcaat gatacgacac tggttcttgt gaacgcaatc 540
tattttcaaag ggcagtggga gaataaatTTT aaaaaagaaa acactaaaga ggaaaaattt 600
tggccaaaca agaatacata caartcyrra cagatgatga ggcaatacam wtcytttmat 660
tttgctygc tggaggatgt acaggccaag gtcttggaat taccatacaa aggcaaagat 720
ctaagcatga ttgtgytgct gccaaatgaa atcgatggtc tscagaagct tgaagagaaa 780
ctcactgctg agaaattgat ggaatggaca agtttgcaga atatgagaga gacaygtgtc 840
gatttacact tacctcggtt caaartggaa gagagctatg acctcaagga cacgttgaga 900
accatgggaa tgggtratat cttcaatggg gatgcagacc tctcaggcat gacckggagc 960
crcggtctck yrstatctrr agtcctacac aaggcctttg tggaggtyac wgaggaggga 1020
gyrgaagctg cagctgccac cgctgtagta ggattcggat catcacctac ttcaactaat 1080
gaagagttcc attgtaatca ccctttccta ttcttcataa ggcaaaaataa gaccaacagc 1140
atcctcttct atggcagatt ctcacccccg tag 1173

```

<210> 19

<211> 390

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic construct

<220>

<221> MOD_RES

<222> (210)

<223> Ile or Val

<220>

<221> MOD_RES

<222> (217)

<223> Thr or Asn

<220>

<221> MOD_RES

<222> (220)

<223> His or Asn

<220>

<221> MOD_RES

<222> (223)

<223> Ser or Leu

<220>

<221> MOD_RES

<222> (279)

<223> Arg or Cys

<220>

<221> MOD_RES

<222> (289)

<223> Val or Met

<220>
 <221> MOD_RES
 <222> (306)
 <223> Asp or Asn

<220>
 <221> MOD_RES
 <222> (319)
 <223> Gly or Trp

<220>
 <221> MOD_RES
 <222> (321)
 <223> Arg or His

<220>
 <221> MOD_RES
 <222> (324)
 <223> Val or Ser

<220>
 <221> MOD_RES
 <222> (325)
 <223> Leu or Val

<220>
 <221> MOD_RES
 <222> (327)
 <223> Gly or Lys

<220>
 <221> MOD_RES
 <222> (341)
 <223> Ala or Val

<400> 19
 Met Asn Ser Leu Ser Glu Ala Asn Thr Lys Phe Met Phe Asp Leu Phe
 1 5 10 15
 Gln Gln Phe Arg Lys Ser Lys Glu Asn Asn Ile Phe Tyr Ser Pro Ile
 20 25 30
 Ser Ile Thr Ser Ala Leu Gly Met Val Leu Leu Gly Ala Lys Asp Asn
 35 40 45
 Thr Ala Gln Gln Ile Ser Lys Val Leu His Phe Asp Gln Val Thr Glu
 50 55 60
 Asn Thr Thr Glu Lys Ala Ala Thr Tyr His Val Asp Arg Ser Gly Asn
 65 70 75 80
 Val His His Gln Phe Gln Lys Leu Leu Thr Glu Phe Asn Lys Ser Thr
 85 90 95
 Asp Ala Tyr Glu Leu Lys Ile Ala Asn Lys Leu Phe Gly Glu Lys Thr
 100 105 110

Tyr	Gln	Phe	Leu	Gln	Glu	Tyr	Leu	Asp	Ala	Ile	Lys	Lys	Phe	Tyr	Gln	115	120	125
Thr	Ser	Val	Glu	Ser	Thr	Asp	Phe	Ala	Asn	Ala	Pro	Glu	Glu	Ser	Arg	130	135	140
Lys	Lys	Ile	Asn	Ser	Trp	Val	Glu	Ser	Gln	Thr	Asn	Glu	Lys	Ile	Lys	145	150	155
Asn	Leu	Phe	Pro	Asp	Gly	Thr	Ile	Gly	Asn	Asp	Thr	Thr	Leu	Val	Leu	165	170	175
Val	Asn	Ala	Ile	Tyr	Phe	Lys	Gly	Gln	Trp	Glu	Asn	Lys	Phe	Lys	Lys	180	185	190
Glu	Asn	Thr	Lys	Glu	Glu	Lys	Phe	Trp	Pro	Asn	Lys	Asn	Thr	Tyr	Lys	195	200	205
Ser	Xaa	Gln	Met	Met	Arg	Gln	Tyr	Xaa	Ser	Phe	Xaa	Phe	Ala	Xaa	Leu	210	215	220
Glu	Asp	Val	Gln	Ala	Lys	Val	Leu	Glu	Ile	Pro	Tyr	Lys	Gly	Lys	Asp	225	230	235
Leu	Ser	Met	Ile	Val	Leu	Leu	Pro	Asn	Glu	Ile	Asp	Gly	Leu	Gln	Lys	245	250	255
Leu	Glu	Glu	Lys	Leu	Thr	Ala	Glu	Lys	Leu	Met	Glu	Trp	Thr	Ser	Leu	260	265	270
Gln	Asn	Met	Arg	Glu	Thr	Xaa	Val	Asp	Leu	His	Leu	Pro	Arg	Phe	Lys	275	280	285
Xaa	Glu	Glu	Ser	Tyr	Asp	Leu	Lys	Asp	Thr	Leu	Arg	Thr	Met	Gly	Met	290	295	300
Val	Xaa	Ile	Phe	Asn	Gly	Asp	Ala	Asp	Leu	Ser	Gly	Met	Thr	Xaa	Ser	305	310	315
Xaa	Gly	Leu	Xaa	Xaa	Ser	Xaa	Val	Leu	His	Lys	Ala	Phe	Val	Glu	Val	325	330	335
Thr	Glu	Glu	Gly	Xaa	Glu	Ala	Ala	Ala	Ala	Thr	Ala	Val	Val	Gly	Phe	340	345	350
Gly	Ser	Ser	Pro	Ala	Ser	Thr	Asn	Glu	Glu	Phe	His	Cys	Asn	His	Pro	355	360	365
Phe	Leu	Phe	Phe	Ile	Arg	Gln	Asn	Lys	Thr	Asn	Ser	Ile	Leu	Phe	Tyr	370	375	380
Gly	Arg	Phe	Ser	Ser	Pro											385	390	